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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/020,746DATE: 07/14/1999
TIME: 11:04:51

Input Set: I020746.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Ashkenazi, Avi J.
2 Chuntharapai, Anan
3 Kim, Kyung Jin
4 <120> TITLE OF INVENTION: APO-2 RECEPTOR
5 <130> FILE REFERENCE: 11669.28US04
6 <140> CURRENT APPLICATION NUMBER: US/09/020,746
7 <141> CURRENT FILING DATE: 1998-02-09
8 <150> EARLIER APPLICATION NUMBER: 08/857,216
9 <151> EARLIER FILING DATE: 1997-05-15
10 <160> NUMBER OF SEQ ID NOS: 11
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 411
14 <212> TYPE: PRT
15 <213> ORGANISM: Homo sapiens
16 <220> FEATURE:
17 <221> NAME/KEY: VARIANT
18 <222> LOCATION: (410)
19 <223> OTHER INFORMATION: Xaa = Leu or Met
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22 1 5 10 15
23 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
24 20 25 30
25 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
26 35 40 45
27 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
28 50 55 60
29 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
30 65 70 75 80
31 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
32 85 90 95
33 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
34 100 105 110
35 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
36 115 120 125
37 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
38 130 135 140
39 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
40 145 150 155 160
41 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
42 165 170 175
43 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
44 180 185 190

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45 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
46 195 200 205
47 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
48 210 215 220
49 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
50 225 230 235 240
51 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
52 245 250 255
53 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
54 260 265 270
55 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
56 275 280 285
57 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
58 290 295 300
59 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
60 305 310 315 320
61 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
62 325 330 335
63 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
64 340 345 350
65 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
66 355 360 365
67 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
68 370 375 380
69 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
70 385 390 395 400
71 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Xaa Ser
72 405 410

73 <210> SEQ ID NO 2
74 <211> LENGTH: 1799
75 <212> TYPE: DNA
76 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
78 <221> NAME/KEY: variation
79 <222> LOCATION: (1367)
80 <223> OTHER INFORMATION: w = Adenine, Thymine or Uracil
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82 cccacgcgtc cgcataaatc agcacgcggc cggagaaccc cgcaatctct gcgcccacaa 60
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84 aagagcgttc cctaccgcca tggaacaacg gggacagaac gccccggccg cttcgggggc 180
85 ccggaaaagg cacggcccag gaccagggga ggcgcgggga gccaggcctg ggctccgggt 240
86 cccaagacc cttgtgctcg ttgtcgccgc ggtcctgctg ttggtctcag ctgagtctgc 300
87 tctgatcacc caacaagacc tagtcccca gcagagagcg gcccacaac aaaagaggtc 360
88 cagcccctca gagggattgt gtccacctgg acaccatata tcagaagacg gtagagattg 420
89 catctcctgc aaatatggac aggactatag cactcactgg aatgacctcc ttttctgctt 480
90 gcgctgcacc aggtgtgatt caggtgaagt ggagctaagt ccctgcacca cgaccagaaa 540
91 cacagtgtgt cagtgcgaag aaggcacctt ccgggaagaa gattctcctg agatgtgccg 600
92 gaagtgccgc acagggtgtc ccagagggat ggtcaaggtc ggtgattgta caccctggag 660
93 tgacatcgaa tgtgtccaca aagaatcagg catcatcata ggagtcacag ttgcagccgt 720
94 agtcttgatt gtggctgtgt ttgtttgcaa gtctttactg tggaagaaag tccttcctta 780

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95      cctgaaaggc atctgctcag gtgggtgggtg ggaccctgag cgtgtggaca gaagctcaca 840
96      acgacctggg gctgaggaca atgtcctcaa tgagatcgtg agtatcttgc agcccaccca 900
97      ggtccctgag caggaaatgg aagtcaggga gccagcagag ccaacagggt tcaacatggt 960
98      gtcccccggg gagtcagagc atctgctgga accggcagaa gctgaaagggt ctgagaggag 1020
99      gaggctgctg gttccagcaa atgaagggtga tcccactgag actctgagac agtgcttcga 1080
100     tgacttttgca gacttggtgc cttttgactc ctgggagccg ctcatgagga agttgggcct 1140
101     catggacaat gagataaagg tggctaaagc tgaggcagcg ggccacaggg acaccttgta 1200
102     cacgatgctg ataaagtggg tcaacaaaac cgggcgagat gcctctgtcc acacctgtct 1260
103     ggatgccttg gagacgctgg gagagagact tgccaagcag aagattgagg accacttggt 1320
104     gagctctgga aagttcatgt atctagaagg taatgcagac tctgccwtgt cctaagtgtg 1380
105     attctcttca ggaagtgaga ctttccctgg ttacctttt ttctggaaaa agcccaactg 1440
106     gactccagtc agtaggaaag tgccacaatt gtcacatgac cgggtactgga agaaactctc 1500
107     ccatccaaca tcacccagtg gatggaacat cctgtaactt ttcactgcac ttggcattat 1560
108     ttttataagc tgaatgtgat aataaggaca ctatggaaat gtctggatca ttccgtttgt 1620
109     gcgtactttg agatttggtt tgggatgtca ttgttttcac agcacttttt tatcctaagt 1680
110     taaatgcttt atttatttat ttgggctaca ttgtaagatc catctacaaa aaaaaaaaaa 1740
111     aaaaaaaaaa ggcggccgcg actctagagt cgacctgcag aagcttggcc gccatggcc 1799
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113     <211> LENGTH: 70
114     <212> TYPE: DNA
115     <213> ORGANISM: Artificial Sequence
116     <220> FEATURE:
117     <221> NAME/KEY: misc_feature
118     <222> LOCATION: (1)..(70)
119     <223> OTHER INFORMATION: Sequence is synthesized
120     <400> SEQUENCE: 3
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122     aggcagcggg                                     70
123     <210> SEQ ID NO 4
124     <211> LENGTH: 29
125     <212> TYPE: DNA
126     <213> ORGANISM: Artificial Sequence
127     <220> FEATURE:
128     <221> NAME/KEY: misc_feature
129     <222> LOCATION: (1)..(29)
130     <223> OTHER INFORMATION: Sequence is synthesized
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132     atcagggact ttccgctggg gactttccg                                     29
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134     <211> LENGTH: 30
135     <212> TYPE: DNA
136     <213> ORGANISM: Artificial Sequence
137     <220> FEATURE:
138     <221> NAME/KEY: misc_feature
139     <222> LOCATION: (1)..(30)
140     <223> OTHER INFORMATION: Sequence is synthesized
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142     aggatgggaa gtgtgtgata tacccttgat                                     30
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144     <211> LENGTH: 411

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145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
147 <400> SEQUENCE: 6
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150 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
151      20          25          30
152 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
153      35          40          45
154 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
155      50          55          60
156 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
157      65          70          75          80
158 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
159      85          90          95
160 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
161      100         105         110
162 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
163      115         120         125
164 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
165      130         135         140
166 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
167      145         150         155         160
168 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
169      165         170         175
170 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
171      180         185         190
172 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
173      195         200         205
174 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
175      210         215         220
176 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
177      225         230         235         240
178 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
179      245         250         255
180 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
181      260         265         270
182 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
183      275         280         285
184 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
185      290         295         300
186 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
187      305         310         315         320
188 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
189      325         330         335
190 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
191      340         345         350
192 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
193      355         360         365
194 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu

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195          370          375          380
196      Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
197          385          390          395          400
198      Tyr Leu Glu Gly Asn Ala Asp Ser Ala Leu Ser
199          405          410
200      <210> SEQ ID NO 7
201      <211> LENGTH: 76
202      <212> TYPE: PRT
203      <213> ORGANISM: Homo sapiens
204      <400> SEQUENCE: 7
205      Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys
206          1          5          10          15
207      Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala
208          20          25          30
209      Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys
210          35          40          45
211      Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
212          50          55          60
213      Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp
214          65          70          75
215      <210> SEQ ID NO 8
216      <211> LENGTH: 76
217      <212> TYPE: PRT
218      <213> ORGANISM: Homo sapiens
219      <400> SEQUENCE: 8
220      Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met Arg Gln
221          1          5          10          15
222      Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly Thr Ala
223          20          25          30
224      Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val Asn Lys
225          35          40          45
226      Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu Glu Arg
227          50          55          60
228      Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp
229          65          70          75
230      <210> SEQ ID NO 9
231      <211> LENGTH: 74
232      <212> TYPE: PRT
233      <213> ORGANISM: Homo sapiens
234      <400> SEQUENCE: 9
235      Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
236          1          5          10          15
237      Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile Gly
238          20          25          30
239      Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln
240          35          40          45
241      Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly
242          50          55          60
243      Leu Asp Gly Cys Val Glu Asp Leu Arg Ser
244          65          70

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VERIFICATION SUMMARY
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Line	? Error/Warning	Original Text
71	W "N" or "Xaa" used: Feature required	Tyr Leu Glu Gly Asn Ala Asp Ser Ala Xaa S